

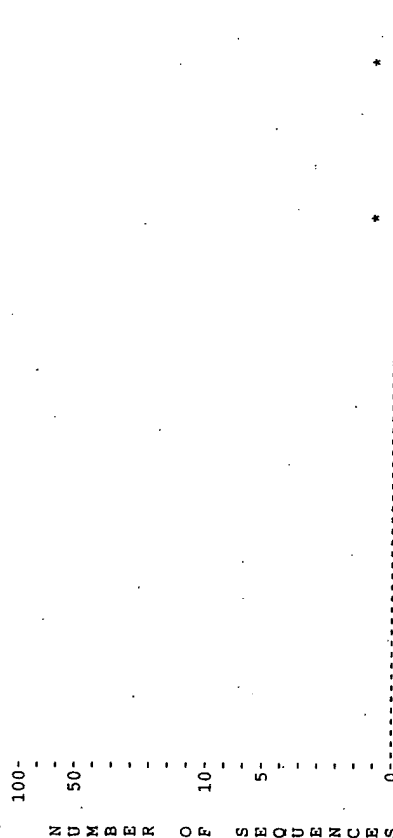
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Of 10, IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file us-09-125-005-6.res made by sdauid on Thu 2 Aug 101 10:06:27-PDT.

Query sequence being compared: US-09-125-005-6 (1-636)  
Number of sequences searched: 2  
Number of scores above cutoff: 2

Results of the initial comparison of US-09-125-005-6 (1-636) with:  
File: PCTUS9914057.pcp



PARAMETERS

Similarity matrix PAM-150 K-tuple 2  
Threshold level of sim. 16%  
Mismatch penalty 1 Joining penalty 20  
Gap penalty 1.00 Window size 32  
Gap size penalty 0.05  
Cutoff score 0  
Randomization group 0

SEARCH STATISTICS

Scores: Mean 564 Median 493 Standard Deviation 101.82  
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 1135  
Number of sequences searched: 2  
Number of scores above cutoff: 2

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name Description Length Score Score Init. Opt. Frame

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1. PCT-US99-14057-1 Sequence 1, Application P 636 636 0.71 0  
The list of other best scores is:  
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Sequence Name Description Length Score Score Init. Opt. Frame  
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2. PCT-US99-14057-2 Sequence 2, Application P 499 492 494 -0.71 0

1. US-09-125-005-6 (1-636)  
PCT-US99-14057-1 Sequence 1, Application PC/TUS9914057

Sequence 1, Application PC/TUS9914057  
GENERAL INFORMATION:

APPLICANT: El-Deiry, Wafik  
TITLE OF INVENTION: Compositions and Methods for Inducing Apoptosis in E6-Express-  
FILE REFERENCE: Penn K-1824  
CURRENT APPLICATION NUMBER: PCT/US99/14057  
CURRENT FILING DATE: 1999-06-23  
EARLIER APPLICATION NUMBER: 60/090,526  
EARLIER FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1

LENGTH: 636  
TYPE: PRT

ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:

AUTHORS: Kaghad, M.; Bonnet, H.; Yang, A.; Creancier, L.; B  
TITLE: Monoallelically expressed gene related to p53 at 1  
JOURNAL: Cell  
VOLUME: 90  
ISSUE: 4  
PAGES: 809-819  
DATE: 1997-08-22  
DATABASE ACCESSION NUMBER: Genbank Y11416  
DATABASE ENTRY DATE: 1997-09-02

Initial Score = 636 Optimized Score = 636 Significance = 0.71  
Residue Identity = 100% Matches = 636 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70  
MAQSTATSPDGGTTTTEHLWSSLEPDSTYFDLPQSSRGNNVVGTDSSMDVHLEGMTTSYMAQFNLLSSTM  
MAQSTATSPDGGTTTTEHLWSSLEPDSTYFDLPQSSRGNNVVGTDSSMDVHLEGMTTSYMAQFNLLSSTM  
X 10 20 30 40 50 60 70

DOMSRAASAPYTPPEHAASVPTHTSPYAQPSSTEDTMSAPVPSNTDYPGPHHFEVTFQSSSTAKSATWTY  
DOMSRAASAPYTPPEHAASVPTHTSPYAQPSSTEDTMSAPVPSNTDYPGPHHFEVTFQSSSTAKSATWTY  
X 80 90 100 110 120 130 140

SPLLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPVYKKAHEVTDVVKRCNPNHGLGRDFNEGOSAPASHLIR  
SPLLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPVYKKAHEVTDVVKRCNPNHGLGRDFNEGOSAPASHLIR  
X 150 160 170 180 190 200 210

VEGNNLSQYDDPVTGROSVVVYEPFQVGTFTILYNFMCNSSCVGGMNRRPILIIITLKRQGVGLGR  
VEGNNLSQYDDPVTGROSVVVYEPFQVGTFTILYNFMCNSSCVGGMNRRPILIIITLKRQGVGLGR  
X 220 230 240 250 260 270 280

SFEGRICACPDGRDKADEDHVREQQALNESSAKNGAASKRAFKQSPPAVFPALGAGVKKRRHGDEDTYYLQVR  
SFEGRICACPDGRDKADEDHVREQQALNESSAKNGAASKRAFKQSPPAVFPALGAGVKKRRHGDEDTYYLQVR  
X 290 300 310 320 330 340 350 360

US-09-125-005-6 (1-636)  
PCT-US99-14057-2 Sequence 2, Application PC/TUS9914057

Initial Score	492	Optimized Score	.494	Significance	-0.71		
Residue Identity	98%	Matches	494	Mismatches	5		
Indels	0	Conservative Substitutions			0		
X	10	20	30	40	50	60	70
MAQSTATSPDGGTTFEHLWSSLEPDSYFDLPQSSRGNNVEVGTSSMDVFHLEGMTTSVMAQFNLLSSTM							
MAQSTATSPDGGTTFEHLWSSLEPDSYFDLPQSSRGNNVEVGTSSMDVFHLEGMTTSVMAQFNLLSSTM							
X	10	20	30	40	50	60	70
DOMSRRASASPYTPEHAASVPTHSPTAQPSSTFDHNSPAPVPSNTDTPGPHHFTVTFQQSSTAKSATWTV							
DOMSRRASASPYTPEHAASVPTHSPTAQPSSTFDHNSPAPVPSNTDTPGPHHFTVTFQQSSTAKSATWTV							
X	80	90	100	110	120	130	140
DOMSRRASASPYTPEHAASVPTHSPTAQPSSTFDHNSPAPVPSNTDTPGPHHFTVTFQQSSTAKSATWTV							
DOMSRRASASPYTPEHAASVPTHSPTAQPSSTFDHNSPAPVPSNTDTPGPHHFTVTFQQSSTAKSATWTV							
X	80	90	100	110	120	130	140
DOMSRRASASPYTPEHAASVPTHSPTAQPSSTFDHNSPAPVPSNTDTPGPHHFTVTFQQSSTAKSATWTV							
DOMSRRASASPYTPEHAASVPTHSPTAQPSSTFDHNSPAPVPSNTDTPGPHHFTVTFQQSSTAKSATWTV							
X	150	160	170	180	190	200	210
SPLLKKLXCOIAKCTPIQIKVSTPPPTGCTAIRAMPVTKKAEHVDVVVKRCNHELGRDFNEQGSAPASHLIR							